Gene signature predicts oral cancer recurrence

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Oral Squamous Cell Carcinoma (OSCC) is responsible for nearly a quarter of all head and neck cancers. It is one of the leading causes of cancer death - largely due to the failure of current histological procedures in predicting the recurrence of the disease. New research published in BioMed Central's open access journal *BMC Cancer* shows that a four-gene signature may accurately predict which patients are at higher risk of OSCC recurrence.

A team of researchers, including Drs. Patricia Reis and Levi Waldron, and led by Dr Suzanne Kamel-Reid and Dr. Igor Jurisica, from the Ontario Cancer Institute at University Health Network (UHN) Toronto, Canada collected cancerous and noncancerous oral tissue samples from patients with OSCC from Toronto General Hospital at UHN. They then used a meta-analysis of five published microarray studies along with their own microarray analysis to reliably identify 138 genes commonly over-expressed in both OSCC and normal margin tissues. Of these genes, a four-gene signature with the highest predictive risk of recurrence was selected. This signature contained cell invasion related genes MMP1, COL4A1, P4HA2 and THBS2.

The researchers explained, "Our data suggest that histologically normal surgical resection margins that over-express MMP1, COL4A1, THBS2 and P4HA2 are indicative of an increased risk of recurrence in OSCC. Patients at higher risk of recurrence could potentially benefit from closer disease monitoring and/or adjuvant post-operative radiation treatment, even in the absence of other clinical and histopathological indicators.
Our findings may be applied to develop a molecular test, which could be clinically useful to help predict which patients are at a higher risk of local recurrence.


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